

# ESTIMATE OF GENETIC PARAMETERS AND PREDICTED GAINS WITH EARLY SELECTION OF PHYSIC NUT FAMILIES

## Estimativa de parâmetros genéticos e ganhos preditos com a seleção precoce de famílias de Pinhão-Manso

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### ABSTRACT

An initial evaluation of early selection of physic nut genotypes based on phenotypic data is presented. In order to predict the genetic gains with early selection, genetic parameters, e.g. additive genetic variance, were first obtained for grain yield along with other numerous traits. The results demonstrated that additive genetic variance exists not only for grain yield, which is considered to be the most important trait for oil and biodiesel production, but also for numerous other traits. The predicted genetic gains for grain yield, considering the selection of the 30, 20, 10 and 5 best families in the second crop year are respectively, 40.47, 48.43, 61.78 and 70.28%. With the selection of highly yielding physic nut genotypes indirectly genotypes with enhanced volume would be also selected, because yield exhibits moderate to high genetic correlations with height e canopy volume. The results here presented demonstrate the potential of the population gathered in the Brazilian physic nut germplasm bank for genetic breeding purposes and that superior physic nut families can be selected with high accuracy based on the evaluation of its second crop.

**Index terms:** *Jatropha curcas* L., reproductive, vegetative traits, plant breeding.

### RESUMO

Uma avaliação inicial da seleção precoce de genótipos baseados em dados fenotípicos é apresentada aqui. Para predizer os ganhos genéticos com a seleção precoce, parâmetros genéticos, e.g. variância genética aditiva, foram obtidos para a produção de grãos e vários outros caracteres. Os resultados demonstram que variância genética aditiva existe, não apenas para produção de grãos, que é considerada a característica mais importante para produção de óleo e biodiesel, mas também para outras características. Os ganhos genéticos preditos com a seleção das 30, 20, 10 e 5 melhores famílias no segundo ano de avaliação são respectivamente 40,47, 48,43, 61,78 e 70,28%. Com a seleção de genótipos mais produtivos de pinhão manso, indiretamente genótipos com elevado volume também serão selecionados, uma vez que a produção exibe correlação alta a moderada com altura e volume de copa. Conjuntamente, os resultados aqui apresentados demonstram o potencial da população representada no banco ativo de germoplasma de pinhão manso brasileiro, para fins de melhoramento e que famílias superiores de pinhão manso podem ser selecionadas com alta acurácia baseada na avaliação da segunda produção.

**Termos para indexação:** *Jatropha curcas* L., reprodutivos, caracteres vegetativos, melhoramento vegetal.

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### INTRODUCTION

Due to the fact that its oil can be converted into biodiesel, either by chemical (BERCHMANS; HIRATA, 2008) or by biological transesterification reactions (MODI et al., 2007), physic nut (*Jatropha curcas* L.) has been considered a potential crop to meet the Brazilian National Program for Production and Use of Biodiesel (LAVIOLA et al., 2010; GURGEL et al., 2011). Current estimates indicate that an area of over 26,000 ha is planted with *J. curcas* in Brazil (ROSADO et al., 2010) even though no elite cultivars are available (CARELS, 2009; DURÃES et al., 2011). As this area is expected to rapidly increase in the forthcoming

years, not only in Brazil but globally, groups involved in physic nut research are now directing efforts to the genetic improvement of the species (ACHTEN et al., 2010; DIVAKARA et al., 2010; ROSADO et al., 2010). In this context, aiming future breeding efforts, a germplasm bank with near 200 accessions was assembled and initially characterized in Brazil (LAVIOLA et al., 2010; ROSADO et al., 2010). This germplasm bank is one of the largest established in the world, and represents most of the genetic variability of the species in Brazil (ROSADO et al., 2010). The initial characterization of this germplasm, using phenotypic (LAVIOLA et al., 2010; LAVIOLA et al., 2011) and molecular data (ROSADO et al., 2010), indicated that,

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although limited, there is genetic variability available for breeding purposes.

Physic nut breeding is only in its initial stages (CARELS, 2009), and initial studies have indicated that intra-populational recurrent selection would be the most suitable way, to rapidly improve the frequency of favorable alleles for traits of interest. Intra-populational recurrent selection can be then considered as a general physic nut breeding approach (LAVIOLA et al., 2012). Based on estimates of genetic correlations among the traits of interest, it seems that breeding efforts should initially be use track trees with increased stem diameter, elevated number of branches and canopy volume so as to increase the chances of finding an exceptionally highly productive tree (LAVIOLA et al., 2010). However, as no elite cultivars are currently available, and because breeding approaches based on recurrent selection of elite genotypes are only on its initial stages, rapid development and release of improved physic nut cultivars is highly desirable. In that context, an initial evaluation of the precision and accuracy of early selection based on phenotypic data could indicate if the selection of superior genotypes in a germplasm bank could be performed efficiently, so as to allow the rapid release of improved physic nut genotypes. A number of studies have undoubtedly demonstrated the benefits of early selection, especially in forest trees and perennial plant species (MARQUES JUNIOR et al., 1996; BAUDOIN et al., 1997; APIOLAZA, 2009), which in general breeding cycles are only completed after many years. In such species, innumerable efforts and approaches are currently being tested in order to reduce the time needed to complete a breeding cycle, including the use of molecular markers in marker assisted selection (MAS) (GRATTAPAGLIA; KIRST, 2008) and genomic selection (GS) (GRATTAPAGLIA; RESENDE, 2010).

The purpose of this study was to (i) estimate genetic parameters for a number of reproductive and vegetative traits of physic nut (based on phenotypic evaluation of developing plants that compose the Brazilian physic nut germplasm bank) and using such parameters to (ii) predict the genetic gains that could be achieved with early selection of the families for yield. Tangentially the study also intended to gather data on the (iii) correlation among the reproductive and vegetative traits.

## MATERIAL AND METHODS

One hundred seventy-five accessions of the physic nut germplasm bank were used in the experiment. The germplasm bank is established at the experimental area of the Embrapa Cerrados [Planaltina-DF, Brazil (15°35'30"

south latitude and 47°42'30" west longitude, at 1007 m altitude)].

The experiment was established using a randomized blocks design with two replicates and five plants (10 plants of a same family) per plot arranged in rows (4x2m spacing). Phenotypic evaluations of 175 accessions were performed considering reproductive and vegetative traits, according to the development of the plants (LAVIOLA et al., 2010). The present work presents the results of the second crop year (November 2009 to July 2010). The traits that were evaluated are (i) grain yield (Yield, g), (ii) 100 seeds weight ( $W_{100}$ , g), (iii) number of seeds per fruit (NSF, n), (iv) ratio between endosperm and seed (E/S), (v) seeds length (SL, mm), (vi) seeds width (SW, mm), (vii) seeds thickness (ST, mm), (viii) total number of branches per plant at 0.5 meters ( $TNB_{0.5}$ ), (ix) total number of branches per plant at 1 meter ( $TNB_{1.0}$ ), (x) total number of branches per plant at 1.5 meters ( $TNB_{1.5}$ ) (xi) plant height (height, m), (xii) stem diameter (SD, mm), (xiii) canopy projection on the row ( $CP_R$ , m), (xiv) canopy projection between lines ( $CP_{BL}$ , m), (xv) canopy volume ( $CV$ ,  $m^3$ ), (xvi) juvenility measured by the number of days to the first flowering (NDF, days) and (xvii) height of the first inflorescence (HFI, m). The canopy volume was estimated by approximating the volume of a cylinder with elliptical base using the formula described by Laviola et al. (2010).

As previously (LAVIOLA et al., 2010), although belonging to different sampling sites, the progenies were analyzed together as a single population, because as indicated by Rosado et al. (2010) physic nut plants in Brazil are not structured into subpopulations. Data analysis was then performed using the statistical model 107 of the software SELEGEN-REML/BLUP (FURLANI et al., 2005; RESENDE, 2007), which considers evaluation in one place in randomized block design, progenies of a single population of mixed reproduction and with one cycle of inbreeding and various plants per plot. The genetic model and mixed model equations used to solve it are described in details in Resende (2007).

The estimates of the genetic parameters were obtained based on individual REML (restricted maximum likelihood). These parameters are: ' $V_g$ ' - genetic variance among families (whose additive and dominance components depends upon selfing rate – assumed here as 25%), ' $V_{plot}$ ' - environmental variance between plots, ' $V_e$ ' - residual variance; ' $V_p$ ' - individual phenotypic variance, ' $h_a^2$ ' - individual total heritability (using 3/2 of the additive genetic variance in the numerator, when  $S=0$ ) in the restricted sense, ' $c_{plot}^2$ ' - determination coefficient of plot effect, ' $h_{pm}^2$ ' heritability of the progenies mean (assuming complete survival), 'APS' – accuracy of progeny selection

(assuming complete survival), and ' $h^2_{awp}$ ' - additive heritability within plot (using 1/2 of the additive genetic variance in the numerator, when  $S=0$ ). Means and genetic gains were calculated based on BLUP (best linear unbiased prediction). While computing the genetic gains, the selection of the best families was considered. For the analyses of correlations between the genotypic values, SELEGEN-REML/BLUP model 102, which uses standard procedures previously described (RESENDE, 2007), was adopted. The significance of genetic correlations was tested by the t test (CRUZ, 2006).

## RESULTS AND DISCUSSION

Since estimates of genetic parameters of economically important traits are essential to predict the genetic gains that can be achieved with the selection of superior genotypes, seventeen important traits were calculated and summarized in Tables 1 and 2. Considering the reproductive traits (Table 1) in general, higher proportions of  $V_g/V_p$  and  $V_g/V_{plot}$  were found for yield,  $W_{100}$  and seeds morphology traits (SL, SW and ST), while lower values were found for the traits NSF and E/S. Considering the vegetative traits (Table 2) in general, the higher proportions of  $V_g/V_p$  and  $V_g/V_{plot}$  was found for CV, while mid-values were found for height, SD,  $CP_R$ ,  $CP_{BL}$ , NDF and HFI and low-values for TNB (at 0.5 to 1.5m). These estimates directly reflect the utility of such traits for selection

purposes, as higher additive variance values are essential considering the sexual propagation of superior genotypes. The estimates of the additive genetic variance also reflected on the heritability values of progenies means ( $h^2_{pm}$ ). As can be seen in the tables 1 and 2, the population displayed high heritability for some traits, including grain yield and  $W_{100}$ , indicating that there are good prospects for selecting higher yielding families aiming at oil and biodiesel production (Table 3). Moreover the accuracy of progeny selection (APS) considering these traits are elevated (Tables 1 and 2).

On the other hand, no genetic variability at all was found for NSF, E/S and for TNB, especially at lower heights (Tables 1 and 2), as evidenced by the low heritability values. Based on such information, it is clear that these traits should not be used on the selection of superior genotypes and that the improvement of such traits should be performed by means of management practices instead. Such information also suggests that these variables can be discarded for future genetic evaluations, and that it cannot be used as morphological descriptors, hence it does not allow a clear differentiation of related cultivars. Considering the individual total heritability in the restricted sense ( $h^2_a$ ), the population displayed mid-average heritability values for some traits (Tables 1 and 2) indicating that there are also good prospects for selecting higher yielding individuals within a given family.

Table 1 – Genetic parameter estimates for reproductive traits in *Jatropha* accessions in the second crop year.

Parameter	Yield	$W_{100}$	NSF	E/S	SL	SW	ST
$V_g$	2680.16	9.56	0.0006	0.00003	0.107	0.0527	0.0599
$V_{plot}$	2304.58	6.29	0.0018	0.00013	0.069	0.0399	0.0369
$V_e$	4448.01	19.43	0.0356	0.00068	0.262	0.0745	0.0790
$V_p$	9432.75	35.29	0.0381	0.00084	0.439	0.1672	0.1759
$h^2_a$	0.39	0.37	0.02	0.05	0.33	0.43	0.46
$c^2_{plot}$	0.29	0.17	0.05	0.15	0.16	0.23	0.21
$h^2_{pm}$	0.62	0.65	0.12	0.18	0.63	0.65	0.69
APS	0.79	0.80	0.35	0.43	0.79	0.81	0.83
$h^2_{awp}$	0.22	0.18	0.006	0.017	0.153	0.26	0.28
Mean	176.73	64.79	2.70	0.61	17.67	10.68	8.39
Maximum	782.00	130	3.21	0.87	28.30	16.53	15.44
Minimum	50.10	45	1.63	0.40	14.27	7.45	5.31

$V_g$  - genetic variance among families;  $V_{plot}$  - environmental variance between plots,  $V_e$  - residual variance;  $V_p$  - individual phenotypic variance;  $h^2_a$  - individual total heritability in the restricted sense,  $c^2_{plot}$  - determination coefficient of plot effect,  $h^2_{pm}$  - heritability of the progenies mean, APS - accuracy of progeny selection and  $h^2_{awp}$  - additive heritability within plot. Yield - grain yield,  $W_{100}$  weight of 100 seeds, NSF - number of seeds per fruit, E/S - ratio between endosperm and seed, SL - seeds length, SW - seeds width and ST - seeds thickness.

Table 2 – Genetic parameter estimates for vegetative traits in *Jatropha* accessions in the second crop year.

Parameter	TNB <sub>0.5</sub>	TNB <sub>1.0</sub>	TNB <sub>1.5</sub>	Height	SD	CP <sub>R</sub>	CP <sub>BL</sub>	CV	NDF	HFI
V <sub>g</sub>	0.0618	0.1041	0.6879	0.0124	27.315	0.0157	0.0224	0.5535	45.590	0.0027
V <sub>plot</sub>	0.2940	0.4903	1.4495	0.0086	43.458	0.0107	0.0159	0.3028	49.459	0.0024
V <sub>e</sub>	1.4214	2.0704	4.5625	0.0288	155.94	0.0600	0.0693	1.1168	190.33	0.0132
V <sub>p</sub>	1.7773	2.6649	6.6999	0.0498	226.72	0.0865	0.1077	1.9732	285.38	0.0118
h <sup>2</sup> <sub>a</sub>	0.05	0.05	0.14	0.34	0.16	0.25	0.28	0.38	0.22	0.20
c <sup>2</sup> <sub>plot</sub>	0.16	0.18	0.21	0.17	0.19	0.12	0.14	0.15	0.17	0.13
h <sup>2</sup> <sub>pm</sub>	0.18	0.18	0.37	0.63	0.42	0.58	0.60	0.67	0.51	0.51
APS	0.42	0.43	0.60	0.79	0.65	0.76	0.77	0.82	0.71	0.71
h <sup>2</sup> <sub>awp</sub>	0.016	0.018	0.056	0.161	0.065	0.098	0.12	0.185	0.089	0.076
Mean	4.43	5.12	6.84	2.42	119.51	1.18	1.26	2.98	142.04	1.15
Maximum	13	13	20	3.02	187.04	2.49	2.90	8.47	206	1.58
Minimum	1	1	1	1.43	48.62	0.40	0.40	0.50	100	0.62

V<sub>g</sub> - genetic variance among families; V<sub>plot</sub> - environmental variance between plots, V<sub>e</sub> - residual variance; V<sub>p</sub> - individual phenotypic variance; h<sup>2</sup><sub>a</sub> - individual total heritability in the restricted sense, c<sup>2</sup><sub>plot</sub> - determination coefficient of plot effect, h<sup>2</sup><sub>pm</sub> - heritability of the progenies mean, APS - accuracy of progeny selection and h<sup>2</sup><sub>awp</sub> - additive heritability within plot. TNB 0.5- total number of branches per plant at 0.5 meters, TNB 1.0 - total number of branches per plant at 1 meter, TNB 1.5 - total number of branches per plant at 1.5 meters, SD - stem diameter, CP<sub>R</sub> - canopy projection on the row, CP<sub>BL</sub> - canopy projection between lines, CV - canopy volume, NDF - number of days to the first flowering and HFI - height of the first inflorescence.

It is interesting to note that as morphological contrasting traits are important for certification purposes, identification of useful traits that can be used with such purposes is essential in a breeding program. In this context, given the high heritability values here presented for seed morphology traits i.e. SL, SW and ST (Table 1) such traits may allow the differentiation of physic nut cultivars. It is noteworthy that as these traits are not directly related to grain yield, its usefulness in the selection of superior genotypes is virtually null.

An important concern when performing field experiments is the ideal control of undesirable effects. In this context, the determination coefficient of plot effects (c<sup>2</sup><sub>plot</sub>) is an important parameter to be estimated as it quantifies the variability within blocks, and consequently the degree of experimental control. In the present work, the estimates for such parameter ranged from 0.05 to 0.29 (average 0.18), when considering the reproductive traits and from 0.05 to 0.38 (average 0.16), when considering the vegetative traits (Tables 1 and 2). These results thus indicate low environmental variation among plots within a given block and low environmental correlation of the observations within plot and thus good experimental control.

In order to predict the genetic gains with early selection the genetic parameters were first obtained for grain yield along with other numerous traits. The results

demonstrated that additive genetic variance exists not only for grain yield, which is considered to be the most important trait for oil and biodiesel production, but also for numerous other traits. Laviola et al. (2010) earlier reported the existence of additive genetic variance for grain yield and other traits in this same population (Brazilian germplasm bank) based on the first crop. Even though it was speculated that elevated genetic gains could be obtained with the selection of superior families/individuals in this germplasm bank, no estimates of the genetic gains were presented. Here, such estimates are presented along with the genetic parameters based on the second crop of this population. To the best of our knowledge this is the first report of the genetic gains that can be obtained with early selection of higher yielding genotypes in physic nut germplasm in Brazil, and the most representative report of the genetic correlations between physic nut traits. These information and especially those related to the magnitude of the predicted genetic gains, may be of special interest as it suggests that an alternative physic nut breeding approach can be adopted, at least on the initial stages of the breeding program.

In this context, the predicted genetic gains for grain yield, considering the early selection of different number of families are summarized in table 3. It is notorious that the predicted genetic gains are, most of the times, quite elevated. Such behavior is indeed expected in the initial

stages of a breeding program, because in a context where most of the plants produce very little, the selection of a group of plants that yields higher is indeed expected to provide elevated genetic gains.

Table 3 – Predicted genetic gains considering grain yield (g plant<sup>-1</sup>), with early selection of the best families in the physic nut germplasm bank.

Progeny	a	Gain	New mean	Gain (%)
1	141.06	141.06	317.80	79.82
5	111.58	124.20	300.94	70.28
10*	76.73	109.18	285.92	61.78
20**	45.74	85.59	262.33	48.43
30***	41.63	71.54	248.27	40.47
50****	14.02	52.85	229.59	29.91

\*Selection of the ten best progenies; \*\*Selection of the twenty best progenies; \*\*\*Selection of the thirty best progenies; \*\*\*\*Selection of the fifty best progenies.

The results here presented also demonstrate that superior physic nut families can be selected, with high accuracy (Table 1), based solely on the evaluation of its second crop. This fact probably reflect the elevated heritabilities of progenies means ( $h^2_{pm}$ ) earlier verified for yield (Table 1). In such context and considering that physic nut is perennial plant species, the selection performed based on the information of the second crop can be considered then a form of early selection. Early selection has been demonstrated to benefit genetic breeding programs of forest trees and perennial plant species (MARQUES JUNIOR et al., 1996; BAUDOUIN et al., 1997; APIOLAZA, 2009), as it allow a breeding cycle to be completed faster. Based on the predicted gains here reported, independent of the selection strategy used, in principle two selection cycles could be performed in the same time (i.e. 4-5 years) that only one cycle would be completed based on intra-populational recurrent selection with three consecutive measurements, which is thought to be the most effective method for improving physic nut genotypes.

Independent of the selection strategy to be employed, it is reasonably clear that, given the low genetic variability of this population (Brazilian germplasm bank), the genetic gains will tend to drop fast in the next breeding cycles. This fact reinforces the need of adding more diversity to the germplasm bank by collecting new samples in the center of origin/diversity of the species as early suggested by Rosado et al. (2010) in Brazil and in other

countries by Divakara et al. (2010). These new sources of genetic variability could be later gradually introduced into the base population of the breeding program, so as to assure a wider genetic basis.

Table 4 presents the estimates of genotypic correlations among the seventeen traits measured. Such information is essential for a breeding program as it may allow breeders to predict the indirect genetic gain in one trait based on the selection of another trait. Moreover, it may contribute to the delineation of efficient strategies to maintain the genetic variability in non-selected traits (BHERING et al., 2012). Considering that grain yield is among the most important traits aiming at oil and biodiesel production (SPINELLI et al., 2010; ROCHA et al., 2012), it is important to establish the genotypic correlation of this trait with others. In that context, higher magnitude correlations (of positive direction) were observed between yield and TNB<sub>1.5</sub>, CP<sub>R</sub>, CP<sub>BL</sub> and CV (Table 4). It is interesting to note that the higher correlation (0.5774) was obtained between yield and CV, indicating that plant architecture is an important contributor to productivity. In that context, TNB at 1.5m seems to be a major determinant of plant canopy architecture given the high correlation values found between this trait and CP<sub>R</sub>, CP<sub>BL</sub> and CV (Table 4). The higher correlations however, were obtained between traits that have a direct relationship, e.g. between canopy traits, between W<sub>100</sub> and seeds morphology traits and between TNB at different heights. Correlations of medium to low magnitude were observed between all other traits (Table 4).

As the results of this paper clearly demonstrate the existence of genotypic variability for numerous traits of interest, and that early and accurate selection can be performed based on the second crop data (yield data), it is important to establish the effect of such selection on other non-directly selected traits, and possible indirect gains. Because of the existence of genetic correlations between the physic nut traits (Table 4) it is possible to predict how the selection based on grain yield may affect the other traits. Such information, i.e. the existence and the magnitude of genetic correlations between traits, can be also of great interest as it may allow the construction of selection indexes for multi-traits to be employed in further stages of the physic nut breeding program (LAVIOLA et al., 2010). In that respect, it is interesting to note that with the selection of highly yielding physic nut genotypes indirectly genotypes with enhanced volume would be also selected, because yield exhibits moderate to high genetic correlations with height, SD, TNB<sub>1.5</sub>, CP<sub>R</sub>, CP<sub>BL</sub> and CV. In other perennial species, SD and CV have been shown to be genetically correlated with yield and its components (WALYARO; VANDER VOSSEN, 1979; CILAS et al., 1998; SPINELLI et al., 2010).

Table 4 – Genetic correlations among phenotypic traits (reproductive and vegetative) measured in the second crop year.

Trait	Yield	W <sub>100</sub>	NSF	E/S	SL	SW	ST	TNB <sub>0.5</sub>	TNB <sub>1.0</sub>	TNB <sub>1.5</sub>	Height	SD	CP <sub>R</sub>	CP <sub>BL</sub>	CV	NDF	HFI
Yield	1	-0.076 <sup>ns</sup>	0.198 <sup>*</sup>	-0.049 <sup>ns</sup>	-0.211 <sup>**</sup>	0.007 <sup>ns</sup>	-0.112 <sup>ns</sup>	0.133 <sup>*</sup>	0.219 <sup>**</sup>	0.403 <sup>**</sup>	0.338 <sup>**</sup>	0.301 <sup>**</sup>	0.510 <sup>**</sup>	0.532 <sup>**</sup>	0.577 <sup>**</sup>	-0.071 <sup>ns</sup>	0.118 <sup>ns</sup>
W <sub>100</sub>		1	-0.055 <sup>ns</sup>	0.225 <sup>**</sup>	0.668 <sup>**</sup>	0.540 <sup>**</sup>	0.605 <sup>**</sup>	0.025 <sup>ns</sup>	0.020 <sup>ns</sup>	-0.014 <sup>ns</sup>	0.088 <sup>ns</sup>	0.063 <sup>ns</sup>	0.167 <sup>*</sup>	0.144 <sup>*</sup>	0.159 <sup>*</sup>	0.011 <sup>ns</sup>	0.185 <sup>**</sup>
NSF			1	0.046 <sup>ns</sup>	-0.089 <sup>ns</sup>	-0.056 <sup>ns</sup>	-0.120 <sup>ns</sup>	0.078 <sup>ns</sup>	0.015 <sup>ns</sup>	-0.004 <sup>ns</sup>	0.200 <sup>*</sup>	0.031 <sup>ns</sup>	0.066 <sup>ns</sup>	0.018 <sup>ns</sup>	0.077 <sup>ns</sup>	0.088 <sup>ns</sup>	0.163 <sup>*</sup>
E/S				1	0.128 <sup>*</sup>	0.080 <sup>ns</sup>	0.214 <sup>*</sup>	0.129 <sup>ns</sup>	0.068 <sup>ns</sup>	0.032 <sup>ns</sup>	-0.038 <sup>ns</sup>	0.047 <sup>ns</sup>	0.090 <sup>ns</sup>	0.023 <sup>ns</sup>	0.029 <sup>ns</sup>	-0.085 <sup>ns</sup>	0.011 <sup>ns</sup>
SL					1	0.506 <sup>**</sup>	0.638 <sup>**</sup>	0.040 <sup>ns</sup>	0.043 <sup>ns</sup>	-0.062 <sup>ns</sup>	-0.094 <sup>ns</sup>	-0.085 <sup>ns</sup>	0.027 <sup>ns</sup>	0.039 <sup>ns</sup>	0.024 <sup>ns</sup>	-0.018 <sup>ns</sup>	0.148 <sup>*</sup>
SW						1	0.820 <sup>**</sup>	0.003 <sup>ns</sup>	-0.028 <sup>ns</sup>	-0.056 <sup>ns</sup>	0.155 <sup>*</sup>	0.148 <sup>*</sup>	0.037 <sup>ns</sup>	0.020 <sup>ns</sup>	0.041 <sup>ns</sup>	0.275 <sup>*</sup>	0.179 <sup>**</sup>
ST							1	0.072 <sup>ns</sup>	0.057 <sup>ns</sup>	-0.049 <sup>ns</sup>	0.016 <sup>ns</sup>	0.001 <sup>ns</sup>	0.033 <sup>ns</sup>	-0.006 <sup>ns</sup>	0.006 <sup>ns</sup>	0.127 <sup>ns</sup>	0.135 <sup>ns</sup>
TNB <sub>0.5</sub>								1	0.740 <sup>**</sup>	0.329 <sup>**</sup>	-0.126 <sup>ns</sup>	0.193 <sup>*</sup>	0.100 <sup>ns</sup>	0.150 <sup>ns</sup>	0.105 <sup>ns</sup>	-0.208 <sup>*</sup>	-0.070 <sup>ns</sup>
TNB <sub>1.0</sub>									1	0.633 <sup>**</sup>	-0.193 <sup>**</sup>	0.167 <sup>*</sup>	0.310 <sup>**</sup>	0.323 <sup>**</sup>	0.275 <sup>**</sup>	-0.477 <sup>**</sup>	-0.351 <sup>**</sup>
TNB <sub>1.5</sub>										1	0.071 <sup>ns</sup>	0.348 <sup>**</sup>	0.661 <sup>**</sup>	0.654 <sup>**</sup>	0.633 <sup>**</sup>	-0.433 <sup>**</sup>	-0.240 <sup>**</sup>
Height											1	0.530 <sup>**</sup>	0.386 <sup>**</sup>	0.406 <sup>**</sup>	0.515 <sup>**</sup>	0.274 <sup>*</sup>	0.541 <sup>**</sup>
SD												1	0.433 <sup>**</sup>	0.448 <sup>**</sup>	0.472 <sup>**</sup>	0.079 <sup>ns</sup>	0.167 <sup>*</sup>
CP <sub>R</sub>													1	0.850 <sup>*</sup>	0.937 <sup>**</sup>	-0.228 <sup>*</sup>	0.021 <sup>ns</sup>
CP <sub>BL</sub>														1	0.943 <sup>**</sup>	-0.158 <sup>*</sup>	0.042 <sup>ns</sup>
VC															1	-0.152 <sup>*</sup>	0.115 <sup>*</sup>
NDF																1	0.458 <sup>**</sup>

\* and \*\* significant at 5% and 1% by *t* test respectively; ns, not significant. Yield – grain yield, W<sub>100</sub> – weight of 100 seeds, NSF – number of seeds per fruit, E/S – ratio between endosperm and seed, SL – seeds length, SW – seeds width, ST – seeds thickness, TNB 0.5 – total number of branches per plant at 0.5 meters, TNB 1.0 – total number of branches per plant at 1 meter, TNB 1.5 – total number of branches per plant at 1.5 meters, SD – stem diameter, CP<sub>R</sub> – canopy projection on the row, CP<sub>BL</sub> – canopy projection between lines, CV – canopy volume, NDF – number of days to the first flowering and HFI – height of the first inflorescence.

Generally, the purpose of estimating genetic correlations between traits of interest is to determine which traits can be potentially used as an indirect indicator of higher yielding genotypes, thus allowing indirect selection. However, by looking at the genotypic correlation on the opposite way, one can establish the general features of highly yielding genotypes. For a species like physic nut for which cultural practices are not well established, this information could be very useful to adjust the production system. For example, by determining that higher yielding genotypes are generally those with a specific plant architecture (in the current case it seems that larger and taller plants produce more than smaller plants) a mechanized harvest system can be correctly planned, as well the spacing and nutrient requirement.

### CONCLUSION

The results here presented confirms the existence of genetic variability that may allow genetic breeding of the species and that genetic gains can be achieved with the selection of superior physic nut families based on the evaluation of its second crop.

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